

SEQUENCE LISTING

<110> University of Utah

<120> HEPARIN BINDING PROTEINS: SENSORS FOR
HEPARIN DETECTION

<130> 21101.0041P1

<140> Unassigned

<141> 2004-08-12

<150> 60/494,495

<151> 2003-08-12

<160> 67

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<221> VARIANT

<222> 1,9

<223> Xaa can be Arg or Lys

<221> VARIANT

<222> 2-8

<223> Xaa = basic residues

<400> 1

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 2

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

cgggatccgg tgctagccgt gactcctatg cacagctcct tgg

43

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3

ggagcggtcg acacggatgc ccagagcttt atctaattc

39

<210> 4

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

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caggaagtgg tt

60

72

<210> 5

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

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ccctcgagac cg

60

72

<210> 6

<211> 62

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6

Arg	Asp	Ser	Tyr	Ala	Gln	Leu	Leu	Gly	His	Gln	Asn	Leu	Lys	Gln	Lys
1				5				10						15	
Ile	Lys	His	Val	Val	Lys	Leu	Lys	Asp	Glu	Asn	Ser	Gln	Leu	Lys	Ser
			20					25					30		
Glu	Val	Ser	Lys	Leu	Arg	Ser	Gln	Leu	Val	Lys	Arg	Lys	Gln	Asn	Glu
			35				40					45			
Leu	Arg	Leu	Gln	Gly	Glu	Leu	Asp	Lys	Ala	Leu	Gly	Ile	Arg		
	50					55				60					

<210> 7

<211> 794

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 7

Met 1	Ser	Phe	Pro	Lys 5	Ala	Pro	Leu	Lys	Arg 10	Phe	Asn	Asp	Pro	Ser 15	Gly
Cys	Ala	Pro	Ser	Pro	Gly	Ala	Tyr	Asp	Val	Lys	Thr	Ser	Glu	Ala	Thr
			20					25					30		
Lys	Gly	Pro	Val	Ser	Phe	Gln	Lys	Ser	Gln	Arg	Phe	Lys	Asn	Gln	Arg
		35					40					45			
Glu	Ser	Gln	Gln	Asn	Leu	Ser	Ile	Asp	Lys	Asp	Thr	Thr	Leu	Leu	Ala
	50					55					60				
Ser	Ala	Lys	Lys	Ala	Lys	Lys	Ser	Val	Ser	Lys	Lys	Asp	Ser	Gln	Lys
65					70					75					80
Asn	Asp	Lys	Asp	Val	Lys	Arg	Leu	Glu	Lys	Glu	Ile	Arg	Ala	Leu	Leu
				85					90					95	
Gln	Glu	Arg	Gly	Thr	Gln	Asp	Lys	Arg	Ile	Gln	Asp	Met	Glu	Ser	Glu
			100					105					110		
Leu	Glu	Lys	Thr	Glu	Ala	Lys	Leu	Asn	Ala	Ala	Val	Arg	Glu	Lys	Thr
		115					120					125			
Ser	Leu	Ser	Ala	Ser	Asn	Ala	Ser	Leu	Glu	Lys	Arg	Leu	Thr	Glu	Leu
	130					135					140				
Thr	Arg	Ala	Asn	Glu	Leu	Leu	Lys	Ala	Lys	Phe	Ser	Glu	Asp	Gly	His
145					150					155					160
Gln	Lys	Asn	Met	Arg	Ala	Leu	Ser	Leu	Glu	Leu	Met	Lys	Leu	Arg	Asn
				165					170					175	
Lys	Arg	Glu	Thr	Lys	Met	Arg	Ser	Met	Met	Val	Lys	Gln	Glu	Gly	Met
			180					185					190		
Glu	Leu	Lys	Leu	Gln	Ala	Thr	Gln	Lys	Asp	Leu	Thr	Glu	Ser	Lys	Gly
		195					200					205			
Lys	Ile	Val	Gln	Leu	Glu	Gly	Lys	Leu	Val	Ser	Ile	Glu	Lys	Glu	Lys
	210					215					220				
Ile	Asp	Glu	Lys	Cys	Glu	Thr	Glu	Lys	Leu	Leu	Glu	Tyr	Ile	Gln	Glu
225					230					235					240
Ile	Ser	Cys	Ala	Ser	Asp	Gln	Val	Glu	Lys	Cys	Lys	Val	Asp	Ile	Ala
				245					250					255	
Gln	Leu	Glu	Glu	Asp	Leu	Lys	Glu	Lys	Asp	Arg	Glu	Ile	Leu	Ser	Leu
			260					265					270		
Lys	Gln	Ser	Leu	Glu	Glu	Asn	Ile	Thr	Phe	Ser	Lys	Gln	Ile	Glu	Asp
		275					280					285			
Leu	Thr	Val	Lys	Cys	Gln	Leu	Leu	Glu	Thr	Glu	Arg	Asp	Asn	Leu	Val
	290					295					300				
Ser	Lys	Asp	Arg	Glu	Arg	Ala	Glu	Thr	Leu	Ser	Ala	Glu	Met	Gln	Ile
305					310					315					320
Leu	Thr	Glu	Arg	Leu	Ala	Leu	Glu	Arg	Gln	Glu	Tyr	Glu	Lys	Leu	Gln
				325					330					335	
Gln	Lys	Glu	Leu	Gln	Ser	Gln	Ser	Leu	Leu	Gln	Gln	Glu	Lys	Glu	Leu
			340					345					350		
Ser	Ala	Arg	Leu	Gln	Gln	Gln	Leu	Cys	Ser	Phe	Gln	Glu	Glu	Met	Thr

Glu Ser Glu Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser Leu Arg Asp
 485 490 495
 Val Thr Ala Gln Leu Glu Ser Glu Gln Glu Lys Tyr Asn Asp Thr Ala
 500 505 510
 Gln Ser Leu Arg Asp Val Thr Ala Gln Leu Glu Ser Val Gln Glu Lys
 515 520 525
 Tyr Asn Asp Thr Ala Gln Ser Leu Arg Asp Val Ser Ala Gln Leu Glu
 530 535 540
 Ser Tyr Lys Ser Ser Thr Leu Lys Glu Ile Glu Asp Leu Lys Leu Glu
 545 550 555 560
 Asn Leu Thr Leu Gln Glu Lys Val Ala Met Ala Glu Lys Ser Val Glu
 565 570 575
 Asp Val Gln Gln Gln Ile Leu Thr Ala Glu Ser Thr Asn Gln Glu Tyr
 580 585 590
 Ala Arg Met Val Gln Asp Leu Gln Asn Arg Ser Thr Leu Lys Glu Glu
 595 600 605
 Glu Ile Lys Glu Ile Thr Ser Ser Phe Leu Glu Lys Ile Thr Asp Leu
 610 615 620
 Lys Asn Gln Leu Arg Gln Gln Asp Glu Asp Phe Arg Lys Gln Leu Glu
 625 630 635 640
 Glu Lys Gly Lys Arg Thr Ala Glu Lys Glu Asn Val Met Thr Glu Leu
 645 650 655
 Thr Met Glu Ile Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Glu
 660 665 670
 Lys Thr Lys Pro Phe Gln Gln Gln Leu Asp Ala Phe Glu Ala Glu Lys
 675 680 685
 Gln Ala Leu Leu Asn Glu His Gly Ala Thr Gln Glu Gln Leu Asn Lys
 690 695 700
 Ile Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln
 705 710 715 720
 Lys Ile Lys His Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys
 725 730 735
 Ser Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn
 740 745 750
 Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg His
 755 760 765
 Phe Asp Pro Ser Lys Ala Phe Cys His Ala Ser Lys Glu Asn Phe Thr
 770 775 780
 Pro Leu Lys Glu Gly Asn Pro Asn Cys Cys
 785 790

<210> 8
 <211> 3539
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 8
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 tctccgggtg cttatgatgt taaaacttca gaagcaacta aaggaccagt gtcttttcag 180
 aatcacaaa gatttaaaaa ccaaagagag tctcaacaaa atcttagcat tgacaaagat 240
 acaaccttgc ttgcttcggc taaaaaagca aagaagtctg tgtcaaagaa ggactctcag 300
 aagaatgata aagatgtgaa gagattagaa aaagagattc gcgctctttt gcaagagcga 360
 gggactcagg acaaacggat ccaggacatg gaatctgaat tggagaagac agaagcaaag 420
 ctcaatgcag cagtcagaga gaaaacatct ctctctgcga gtaatgcttc actggaaaaa 480
 cggcttactg aattaaccag agccaacgag ctactaaagg ctaagttttc tgaagatggg 540
 caccaaaaga atatgagagc tctaagcctg gaattgatga aactcagaaa taagagagag 600

acaaagatga	ggagtatgat	ggtcaaacag	gaaggcatgg	agctgaagct	gcaggccact	660
cagaaggacc	tcacggagtc	taagggaaaa	atagtccagc	tggagggaaa	gcttggttca	720
atagagaaa	aaaagatcga	tgaaaaatgt	gaaacagaaa	aactccttaga	atacatccaa	780
gaaattagct	gtgcatctga	tcaagtggaa	aaatgcaaag	tagatattgc	ccagttagaa	840
gaagatttga	aagagaagga	tcgtgagatt	ttaagtctta	agcagtctct	tgaggaaaac	900
attacatttt	ctaagcaaat	agaagacctg	actgttaaat	gccagctact	tgaaacagaa	960
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atcctgacag	agaggctggc	tctggaaaag	caagaatatg	aaaagctgca	acaaaaagaa	1080
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aaatcaaact	acaacctcaa	acgtctggga	ccctccaagg	gcttgggtca	cttctctagc	3300
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<210> 9

<211> 631

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 9

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Met Arg Ala Leu Ser Leu Glu Leu Met Lys Leu Arg Asn Lys Arg Glu
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Thr Lys Met Arg Ser Met Met Val Lys Gln Glu Gly Met Glu Leu Lys
 20          25          30
Leu Gln Ala Thr Gln Lys Asp Leu Thr Glu Ser Lys Gly Lys Ile Val
 35          40          45
Gln Leu Glu Gly Lys Leu Val Ser Ile Glu Lys Glu Lys Ile Asp Glu
 50          55          60
Lys Cys Glu Thr Glu Lys Leu Leu Glu Tyr Ile Gln Glu Ile Ser Cys
 65          70          75          80
Ala Ser Asp Gln Val Glu Lys Cys Lys Val Asp Ile Ala Gln Leu Glu
 85          90          95
Glu Asp Leu Lys Glu Lys Asp Arg Glu Ile Leu Ser Leu Lys Gln Ser
100          105          110
Leu Glu Glu Asn Ile Thr Phe Ser Lys Gln Ile Glu Asp Leu Thr Val
115          120          125
Lys Cys Gln Leu Leu Glu Thr Glu Arg Asp Asn Leu Val Ser Lys Asp
130          135          140
Arg Glu Arg Ala Glu Thr Leu Ser Ala Glu Met Gln Ile Leu Thr Glu
145          150          155          160
Arg Leu Ala Leu Glu Arg Gln Glu Tyr Glu Lys Leu Gln Gln Lys Glu
165          170          175
Leu Gln Ser Gln Ser Leu Leu Gln Gln Glu Lys Glu Leu Ser Ala Arg
180          185          190
Leu Gln Gln Gln Leu Cys Ser Phe Gln Glu Glu Met Thr Ser Glu Lys
195          200          205
Asn Val Phe Lys Glu Glu Leu Lys Leu Ala Leu Ala Glu Leu Asp Ala
210          215          220
Val Gln Gln Lys Glu Glu Gln Ser Glu Arg Leu Val Lys Gln Leu Glu
225          230          235          240
Glu Glu Arg Lys Ser Thr Ala Glu Gln Leu Thr Arg Leu Asp Asn Leu
245          250          255
Leu Arg Glu Lys Glu Val Glu Leu Glu Lys His Ile Ala Ala His Ala
260          265          270
Gln Ala Ile Leu Ile Ala Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser
275          280          285
Leu Arg Asp Val Thr Ala Gln Leu Glu Ser Val Gln Glu Lys Tyr Asn
290          295          300
Asp Thr Ala Gln Ser Leu Arg Asp Val Thr Ala Gln Leu Glu Ser Glu
305          310          315          320
Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser Leu Arg Asp Val Thr Ala
325          330          335
Gln Leu Glu Ser Glu Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser Leu
340          345          350
Arg Asp Val Thr Ala Gln Leu Glu Ser Val Gln Glu Lys Tyr Asn Asp
355          360          365
Thr Ala Gln Ser Leu Arg Asp Val Ser Ala Gln Leu Glu Ser Tyr Lys
370          375          380
Ser Ser Thr Leu Lys Glu Ile Glu Asp Leu Lys Leu Glu Asn Leu Thr
385          390          395          400
Leu Gln Glu Lys Val Ala Met Ala Glu Lys Ser Val Glu Asp Val Gln
405          410          415
Gln Gln Ile Leu Thr Ala Glu Ser Thr Asn Gln Glu Tyr Ala Arg Met
420          425          430
Val Gln Asp Leu Gln Asn Arg Ser Thr Leu Lys Glu Glu Glu Ile Lys
435          440          445
Glu Ile Thr Ser Ser Phe Leu Glu Lys Ile Thr Asp Leu Lys Asn Gln
450          455          460

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Leu Arg Gln Gln Asp Glu Asp Phe Arg Lys Gln Leu Glu Glu Lys Gly
 465 470 475 480
 Lys Arg Thr Ala Glu Lys Glu Asn Val Met Thr Glu Leu Thr Met Glu
 485 490 495
 Ile Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Glu Lys Thr Lys
 500 505 510
 Pro Phe Gln Gln Gln Leu Asp Ala Phe Glu Ala Glu Lys Gln Ala Leu
 515 520 525
 Leu Asn Glu His Gly Ala Thr Gln Glu Gln Leu Asn Lys Ile Arg Asp
 530 535 540
 Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys
 545 550 555 560
 His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val
 565 570 575
 Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg
 580 585 590
 Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg His Phe Asp Pro
 595 600 605
 Ser Lys Ala Phe Cys His Ala Ser Lys Glu Asn Phe Thr Pro Leu Lys
 610 615 620
 Glu Gly Asn Pro Asn Cys Cys
 625 630

<210> 10

<211> 3167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10

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gaatagatat	ctgagttctt	atgtttattg	tagttttctg	aagatgggtca	ccaaaagaat	180
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acggagtcta	agggaaaaat	agtcacagctg	gaggggaaagc	ttgtttcaat	agagaaagaa	360
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gcatctgatc	aagtggaaaa	atgcaaagta	gatattgccc	agttagaaga	agatttgaaa	480
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cagtctttga aaattcttaa aatttcaatc cctttaaatt atccaatctc ttttaaaatt 2760
caaagtcttt ttacaattaa aaagtctctt aactgtgggtc tccactaaaa tactttcttc 2820
cttcaagagg gaaaaatatc agggcacagt cacaaacaat taaaagcaaa atcaaaactac 2880
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agcacacaag ttgtcttcta ggctccagat gcctgtactc cactgctgct gctgttcttg 3000
gtactcattt atggtactgg catctccaaa acactgttgt ctttgctgta actaggcttc 3060
accaatagcc tctcataggc tctcttcatt gtgccaagcc tcaaatectt tgaatgaccc 3120
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<210> 11

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11

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Met Gly Gly Gly Val Ser Tyr Val Gly Trp Leu Glu Lys Ser Glu Thr
  1             5             10             15

Glu Lys Leu Leu Glu Tyr Ile Glu Glu Ile Ser Cys Ala Ser Asp Gln
          20          25          30
Val Glu Lys Tyr Lys Leu Asp Ile Ala Gln Leu Glu Glu Asp Leu Lys
          35          40          45
Glu Lys Asp Arg Glu Ile Leu Cys Leu Lys Gln Ser Leu Glu Glu Lys
          50          55          60
Val Ser Phe Ser Lys Gln Ile Glu Asp Leu Thr Val Lys Cys Gln Leu
          65          70          75          80
Leu Glu Ala Glu Arg Asp Asp Leu Val Ser Lys Asp Arg Glu Arg Ala
          85          90          95
Glu Ser Leu Ser Ala Glu Met Gln Val Leu Thr Glu Lys Leu Leu Leu
          100         105         110
Glu Arg Gln Glu Tyr Glu Lys Leu Gln Gln Asn Glu Leu Gln Ser Gln
          115         120         125
Ser Leu Leu Gln Gln Glu Lys Glu Leu Ser Ala His Leu Gln Gln Gln
          130         135         140
Leu Cys Ser Phe Gln Glu Glu Met Thr Ser Glu Arg Asn Val Phe Lys

145             150             155             160
Glu Gln Leu Lys Leu Ala Leu Asp Glu Leu Asp Ala Val Gln Gln Lys
          165             170             175

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Glu Glu Gln Ser Glu Lys Leu Val Lys Gln Leu Glu Glu Glu Thr Lys

180 185 190

Ser Thr Ala Glu Gln Leu Arg Arg Leu Asp Asp Leu Leu Arg Glu Lys

195 200 205

Glu Ile Glu Leu Glu Lys Arg Thr Ala Ala His Ala Gln Ala Thr Val

210 215 220

Ile Ala Gln Glu Lys Tyr Ser Asp Thr Ala Gln Thr Leu Arg Asp Val

225 230 235 240

Thr Ala Gln Leu Glu Ser Tyr Lys Ser Ser Thr Leu Lys Glu Ile Glu

245 250 255

Asp Leu Lys Leu Glu Asn Leu Thr Leu Gln Glu Lys Val Ala Met Ala

260 265 270

Glu Lys Arg Val Glu Asp Val Gln Gln Gln Ile Leu Thr Ala Glu Ser

275 280 285

Thr Asn Gln Glu Tyr Ala Lys Val Val Gln Asp Leu Gln Asn Ser Ser

290 295 300

Thr Leu Lys Glu Ala Glu Ile Lys Glu Ile Thr Ser Ser Tyr Leu Glu

305 310 315 320

Lys Ile Thr Asp Leu Gln Asn Gln Leu Arg Gln Gln Asn Glu Asp Phe

325 330 335

Arg Lys Gln Leu Glu Glu Glu Gly Ala Lys Met Thr Glu Lys Glu Thr

340 345 350

Ala Val Thr Glu Leu Thr Met Glu Ile Asn Lys Trp Arg Leu Leu Tyr

355 360 365

Glu Glu Leu Tyr Asp Lys Thr Lys Pro Phe Gln Gln Gln Leu Asp Ala

370 375 380

Phe Glu Ala Glu Lys Gln Ala Leu Leu Asn Glu His Gly Ala Thr Gln

385 390 395 400

Glu Gln Leu Ser Lys Ile Arg Asp Ser Tyr Ala Gln Leu Leu Gly His

405 410 415

Gln Asn Leu Lys Gln Lys Ile Lys His Val Val Lys Leu Lys Asp Glu

420 425 430

Asn Ser Gln Leu Lys Ser Glu Val Ser Lys Leu Arg Ser Gln Leu Ala

435 440 445

Lys Arg Lys Gln Asn Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala

450 455 460

Leu Gly Ile Arg His Phe Asp Pro Pro Lys Ala Phe Cys His Glu Ser

465 470 475 480

Lys Glu Asn Val Thr Leu Lys Thr Pro Leu Lys Glu Gly Asn Pro Asn

485 490 495

Cys Cys

<210> 12

<211> 2049

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12

aaccagctat	caccaagctc	gataggcttt	tcacctctac	ctaaaaatct	tcccactatt	60
ttgctacata	gacgggttga	ttcatgaaat	tgtttttagg	tagctcgttt	ggtttcgggg	120
ttcttagctt	aaattctttt	tgctaaggat	tttctagtta	attcattatg	caaaaggtac	180
aagggttaat	ctttgcttat	ttttacttta	aattagtctt	tcaccattcc	cttgcggtac	240
tttctctata	gctcctggta	agtaaatctc	tttctccaat	actttttgag	ttaaatgttt	300
tagtttatgg	gggggggggt	tagttatggt	gggttggttg	aaaaatctga	aacagaaaaa	360

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ctcttagaat acatagaaga aattagctgt gcatctgatc aagtggaaaa atacaaacta      420

gatattgccc agttagaaga agatttgaaa gagaaggatc gtgagatttt atgccttaag      480
caatctcttg aggaaaaggt ttccttttct aagcaaatag aagacctgac tgttaaagt      540
cagctgcttg aagcagaaag agatgatctc gtcagcaagg acagagaaag ggctgaaagc      600
ctcagtgtctg agatgcagggt tctaacagag aagctgtctc tagaaaggca agaatatgaa      660
aagctgcaac aaaatgaatt gcaaagccag tcacttctgc agcaagaaaa ggaactgtct      720
gctcatcttc agcagcagct ctgctcattt caagaggaaa tgacctccga gaggaatgtc      780
tttaaagaac agttgaagct tgccctggat gagctggatg ccgtccagca gaaggaggag      840
cagagtgaac agctgggtta acagctagaa gaggaaacga agtcaactgc ggaacagctg      900
aggcggctgg atgatctgct gagagagaaa gaaattgaac tggagaaaag aaccgctgca      960
catgcccagg ccactgtgat tgcgcaagag aagtacagtg acacagcgca gactctgaga     1020
gatgttactg ctgagttaga aagctataag tcatcaacac ttaaagaaat agaagatctt     1080
aaactggaga atttgactct acaagaaaaa gtagccatgg ctgagaaaag ggtagaagat     1140
gttcaacaac aaatattaac agctgagagc acaaatcagg aatatgcaaa ggtgggtcaa     1200
gatttgcaga acagctcaac attgaaagaa gcagaaatta aagaaatcac atcttcatat     1260
cttgagaaaa taactgattt gcaaaatcaa ctccgacaac aaaatgaaga ctttaggaag     1320
cagctggaag aggaaggggc aaaaatgaca gagaaagaaa ctgcagtgcac agaattaacc     1380
atggaaatta ataaatggcg tctcctatat gaagaactgt atgacaaaac taaacctttt     1440
cagcaacaac tggatgcctt cgaagcagag aagcaggcac tgttgaatga acatggtgca     1500
actcaggagc agctaagtaa aatcagagac tcctacgcac agctgcttgg ccaccagaat     1560
ctgaagcaaa aaatcaaaca tgtcgtgaaa ttgaaagatg aaaatagcca actcaaactc     1620
gaggtgtcaa aactccgatc tcagcttgct aaaaggaaac aaaatgagct cagacttcag     1680
ggagaattag ataaagctct gggcatcagg cactttgacc ctccaaaggc tttttgccat     1740
gaatctaagg agaattgtac cctcaagact ccattgaaag aaggcaacc gaactgtgc      1800
tgagtgcagc tgcagggacc gtggaagtgg acgtccaaga tacttgctga agattgttct     1860
cttcattatt cttgatatta tgtttatagt atatattata taatgtattt aatttctact     1920
gcctattctt aggtatatga aacggtaatt caacatttgt tatcaaaatg tattttgaca     1980
ttttattttc tattatgtgt ctccttaatc atcacctgga tcacctcatt ctgaaccatt     2040
gcttggtt      2049

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<210> 13

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13

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Met Ser Phe Pro Lys Ala Pro Leu Lys Arg Phe Asn Asp Pro Ser Gly
 1           5           10          15
Cys Ala Pro Ser Pro Gly Ala Tyr Asp Val Lys Thr Leu Glu Val Leu
          20          25          30
Lys Gly Pro Val Ser Phe Gln Lys Ser Gln Arg Phe Lys Gln Gln Lys
          35          40          45
Glu Ser Lys Gln Asn Leu Asn Val Asp Lys Asp Thr Thr Leu Pro Ala
          50          55          60
Ser Ala Arg Lys Val Lys Ser Ser Glu Ser Lys Ile Arg Val Leu Leu
65          70          75          80
Gln Glu Arg Gly Ala Gln Asp Ser Arg Ile Gln Asp Leu Glu Thr Glu
          85          90          95
Leu Glu Lys Met Glu Ala Arg Leu Asn Ala Ala Leu Arg Glu Lys Thr
          100         105         110
Ser Leu Ser Ala Asn Asn Ala Thr Leu Glu Lys Gln Leu Ile Glu Leu
          115         120         125
Thr Arg Thr Asn Glu Leu Leu Lys Ser Lys Phe Ser Glu Asn Gly Asn
          130         135         140
Gln Lys Asn Leu Arg Ile Leu Ser Leu Glu Leu Met Lys Leu Arg Asn
145         150         155         160

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Lys	Arg	Glu	Thr	Lys	Met	Arg	Gly	Met	Met	Ala	Lys	Gln	Glu	Gly	Met
				165					170					175	
Glu	Met	Lys	Leu	Gln	Val	Thr	Gln	Arg	Ser	Leu	Glu	Glu	Ser	Gln	Gly
			180					185					190		
Lys	Ile	Ala	Gln	Leu	Glu	Gly	Lys	Leu	Val	Ser	Ile	Glu	Lys	Glu	Lys
		195					200					205			
Ile	Asp	Glu	Lys	Ser	Glu	Thr	Glu	Lys	Leu	Leu	Glu	Tyr	Ile	Glu	Glu
	210					215					220				
Ile	Ser	Cys	Ala	Ser	Asp	Gln	Val	Glu	Lys	Tyr	Lys	Leu	Asp	Ile	Ala
225					230					235					240
Gln	Leu	Glu	Glu	Asn	Leu	Lys	Glu	Lys	Asn	Asp	Glu	Ile	Leu	Ser	Leu
				245					250					255	
Lys	Gln	Ser	Leu	Glu	Glu	Asn	Ile	Val	Ile	Leu	Ser	Lys	Gln	Val	Glu
			260					265					270		
Asp	Leu	Asn	Val	Lys	Cys	Gln	Leu	Leu	Glu	Lys	Glu	Lys	Glu	Asp	His
	275						280					285			
Val	Asn	Arg	Asn	Arg	Glu	His	Asn	Glu	Asn	Leu	Asn	Ala	Glu	Met	Gln
	290					295					300				
Asn	Leu	Lys	Gln	Lys	Phe	Ile	Leu	Glu	Gln	Gln	Glu	Arg	Glu	Lys	Leu
305					310					315					320
Gln	Gln	Lys	Glu	Leu	Gln	Ile	Asp	Ser	Leu	Leu	Gln	Gln	Glu	Lys	Glu
				325					330					335	
Leu	Ser	Ser	Ser	Leu	His	Gln	Lys	Leu	Cys	Ser	Phe	Gln	Glu	Glu	Met
			340					345					350		
Val	Lys	Glu	Lys	Asn	Leu	Phe	Glu	Glu	Glu	Leu	Lys	Gln	Thr	Leu	Asp
	355						360					365			
Glu	Leu	Asp	Lys	Leu	Gln	Gln	Lys	Glu	Glu	Gln	Ala	Glu	Arg	Leu	Val
	370					375					380				
Lys	Gln	Leu	Glu	Glu	Glu	Ala	Lys	Ser	Arg	Ala	Glu	Glu	Leu	Lys	Leu
385					390					395					400
Leu	Glu	Glu	Lys	Leu	Lys	Gly	Lys	Glu	Ala	Glu	Leu	Glu	Lys	Ser	Ser
			405					410					415		
Ala	Ala	His	Thr	Gln	Ala	Thr	Leu	Leu	Leu	Gln	Glu	Lys	Tyr	Asp	Ser
			420					425					430		
Met	Val	Gln	Ser	Leu	Glu	Asp	Val	Thr	Ala	Gln	Phe	Glu	Ser	Tyr	Lys
	435						440					445			
Ala	Leu	Thr	Ala	Ser	Glu	Ile	Glu	Asp	Leu	Lys	Leu	Glu	Asn	Ser	Ser
	450					455					460				
Leu	Gln	Glu	Lys	Ala	Ala	Lys	Ala	Gly	Lys	Asn	Ala	Glu	Asp	Val	Gln
465					470					475					480
His	Gln	Ile	Leu	Ala	Thr	Glu	Ser	Ser	Asn	Gln	Glu	Tyr	Val	Arg	Met
			485					490					495		
Leu	Leu	Asp	Leu	Gln	Thr	Lys	Ser	Ala	Leu	Lys	Glu	Thr	Glu	Ile	Lys
			500					505					510		
Glu	Ile	Thr	Val	Ser	Phe	Leu	Gln	Lys	Ile	Thr	Asp	Leu	Gln	Asn	Gln
	515						520					525			
Leu	Lys	Gln	Gln	Glu	Glu	Asp	Phe	Arg	Lys	Gln	Leu	Glu	Asp	Glu	Glu
	530					535					540				
Gly	Arg	Lys	Ala	Glu	Lys	Glu	Asn	Thr	Thr	Ala	Glu	Leu	Thr	Glu	Glu
545					550					555					560
Ile	Asn	Lys	Trp	Arg	Leu	Leu	Tyr	Glu	Glu	Leu	Tyr	Asn	Lys	Thr	Lys
			565					570						575	
Pro	Phe	Gln	Leu	Gln	Leu	Asp	Ala	Phe	Glu	Val	Glu	Lys	Gln	Ala	Leu
			580					585					590		
Leu	Asn	Glu	His	Gly	Ala	Ala	Gln	Glu	Gln	Leu	Asn	Lys	Ile	Arg	Asp
	595						600					605			
Ser	Tyr	Ala	Lys	Leu	Leu	Gly	His	Gln	Asn	Leu	Lys	Gln	Lys	Ile	Lys
	610					615					620				
His	Val	Val	Lys	Leu	Lys	Asp	Glu	Asn	Ser	Gln	Leu	Lys	Ser	Glu	Val
625					630					635					640

Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Lys Gln Ser Glu Thr Lys
 645 650 655
 Leu Gln Glu Glu Leu Asn Lys Val Leu Gly Ile Lys His Phe Asp Pro
 660 665 670
 Ser Lys Ala Phe His His Glu Ser Lys Glu Asn Phe Ala Leu Lys Thr
 675 680 685
 Pro Leu Lys Glu Gly Asn Thr Asn Cys Tyr Arg Ala Pro Met Glu Cys
 690 695 700
 Gln Glu Ser Trp Lys
 705

<210> 14

<211> 2957

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 14

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gccagtcacc ttcagtttct ggagctggcc gtcaacatgt cctttcctaa ggcgcccttg      60
aaacgattca atgacccttc tggttgtgca ccatctccag gtgcttatga tgttaaaaact      120
ttagaagtat tgaaaggacc agtatccttt cagaaatcac aaagatttaa acaacaaaaa      180
gaatctaaac aaaatcttaa tgttgacaaa gatactacct tgacctgttc agctagaaaa      240
gttaagtctt cggaaatcaaa gattcgtggt cttctacagg aacgtgggtgc ccaggacagc      300
cggatccagg atctggaaac tgagttggaa aagatggaag caaggctaaa tgctgcaacta      360
agggaaaaaa catctctctc tgcaaataat gctacactgg aaaaaaactt tattgaattg      420
accaggacta atgaactact aaaatctaag ttttctgaaa atggtaacca gaagaatttg      480
agaattctaa gcttggagtt gatgaaactt agaaacaaaa gagaaacaaa gatgaggggt      540
atgatggcta agcaagaagg catggagatg aagctgcagg tcacccaaag gagtctcgaa      600
gagtctcaag ggaaaatagc ccaactggag ggaaaacttg tttcaataga gaaagaaaag      660
attgatgaaa aatctgaaac agaaaaactc ttggaataca tcgaagaaat tagttgtgct      720
tcagatcaag tggaaaaata caagctagat attgcccagt tagaagaaaa tttgaaagag      780
aagaatgatg aaatttttaag ccttaagcag tctcttgagg agaattattgt tatattatct      840
aaacaagtag aagatctaaa tgtgaaatgt cagctgcttg aaaaagaaaa agaagaccat      900
gtcaacagga atagagaaca caacgaaaat ctaaattgcag agatgcaaaa cttaaaacag      960
aagtttatct ttgaacaaca ggaacgtgaa aagcttcaac aaaaagaatt acaaattgat      1020
tcacttctgc aacaagagaa agaattatct tcgagctctc atcagaagct ctgttctttt      1080
caagaggaaa tgggttaaaga gaagaatctg tttgaggaag aattaaagca aacactggat      1140
gagcttgata aattacagca aaaggaggaa caagctgaaa ggctgggtcaa gcaattggaa      1200
gaggaagcaa aatctagagc tgaagaatta aaactcctag aagaaaagct gaaagggaag      1260
gaggctgaac tggagaaaag tagtgctgct cataccagg ccacctgct tttgcaggaa      1320
aagtatgaca atattttgga aagccttgaa gatgttactg ctcaatttga aagctataaa      1380
gcgttaacag ccagtgagat agaagatctt aagctggaga actcatcatt acaggaaaaa      1440
gcggccaagg ctgggaaaaa tgcagaggat gttcagcatc agattttggc aactgagagc      1500
tcaaatacaag aatatgtaag gatgcttcta gatctgcaga ccaagtcagc actaaaggaa      1560
acagaaatta aagaaatcac agtttctttt cttcaaaaaa taactgattt gcagaaccaa      1620
ctcaagcaac aggaggaaga ctttagaaaa cagctggaag atgaagaagg aagaaaagct      1680
gaaaaagaaa atacaacagc agaattaact gaagaaatta acaagtggcg tctcctctat      1740
gaagaactat ataataaaac aaaacctttt cagctacaac tagatgcttt tgaagtagaa      1800
aaacaggcat tgttgaatga acatggtgca gctcaggaac agctaaataa aataagagat      1860
tcatatgcta aattattggg tcatacagaa ttgaaacaaa aaatcaagca tgttgtgaag      1920
ttgaaagatg aaaatagcca actcaaactc gaagtatcaa aactccgctg tcagcttgct      1980
aaaaaaaaac aaagtgagac aaaacttcaa gaggaattga ataaagttct aggtatcaaa      2040
cactttgatc cttcaaaggc ttttcatcat gaaagtaaag aaaattttgc cctgaagacc      2100
ccattaaaag aaggcaatac aaactgttac cgagctccta tggagtgtca agaatacatg      2160
aagtaaacad ctgagaaacc tgttgaagat tatttcattc gtcttggtgt tattgatgtt      2220
gctgttatta tatttgacat gggatattta taatgttgta tttaatttta actgccaatc      2280
cttaaatatg tgaaaggaac attttttacc aaagtgtctt ttgacatttt attttttctt      2340
gcaaatacct cctcccta at gctcacctt atcacctcat tctgaaccct ttcgctggct      2400

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ttccagctta gaatgcatct catcaactta aaagtcagta tcatattatt atcctcctgt 2460
tctgaaacct tagtttcaag agtctaaacc ccagattctt cagcttgatc ctggagggtct 2520
tttctagtct gagcttcttt agctaggcta aaacacccttg gcttggtatt gcctctactt 2580
tgattctgat aatgctcact tggtcctacc tattatcctt ctacttgacc agttcaaata 2640
agaaataagg acaagcctaa cttcatagaa acctctctat ttttaatcag ttgtttaata 2700
atttacaggt tcttaggctc catcctgttt gtatgaaatt ataactctgt gattggcctt 2760
taagcctgca ttcttaacaa actcttcagt taattcttag atacactaaa aatctgagaa 2820
actctacatg taactatttc ttcagagttt gtcataact gcttgatcgc tgcatgtcta 2880
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caaaaaaaaa aaaaaaa 2957

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<210> 15

<211> 725

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 15 .

Met Ser Phe Pro Lys Ala Pro Leu Lys Arg Phe Asn Asp Pro Ser Gly

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      1             5             10             15
Cys Ala Pro Ser Pro Gly Ala Tyr Asp Val Lys Thr Leu Glu Val Leu
      20             25             30
Lys Gly Pro Val Ser Phe Gln Lys Ser Gln Arg Phe Lys Gln Gln Lys
      35             40             45
Glu Ser Lys Gln Asn Leu Asn Val Asp Lys Asp Thr Thr Leu Pro Ala
      50             55             60
Ser Ala Arg Lys Val Lys Ser Ser Glu Ser Lys Lys Glu Ser Gln Lys
      65             70             75             80
Asn Asp Lys Asp Leu Lys Ile Leu Glu Lys Glu Ile Arg Val Leu Leu
      85             90             95
Gln Glu Arg Gly Ala Gln Asp Arg Arg Ile Gln Asp Leu Glu Thr Glu
      100            105            110
Leu Glu Lys Met Glu Ala Arg Leu Asn Ala Ala Leu Arg Glu Lys Thr
      115            120            125
Ser Leu Ser Ala Asn Asn Ala Thr Leu Glu Lys Gln Leu Ile Glu Leu
      130            135            140
Thr Arg Thr Asn Glu Leu Leu Lys Ser Lys Phe Ser Glu Asn Gly Asn
      145            150            155            160
Gln Lys Asn Leu Arg Ile Leu Ser Leu Glu Leu Met Lys Leu Arg Asn
      165            170            175
Lys Arg Glu Thr Lys Met Arg Gly Met Met Ala Lys Gln Glu Gly Met
      180            185            190
Glu Met Lys Leu Gln Val Thr Gln Arg Ser Leu Glu Glu Ser Gln Gly
      195            200            205
Lys Ile Ala Gln Leu Glu Gly Lys Leu Val Ser Ile Glu Lys Glu Lys
      210            215            220
Ile Asp Glu Lys Ser Glu Thr Glu Lys Leu Leu Glu Tyr Ile Glu Glu
      225            230            235            240
Ile Ser Cys Ala Ser Asp Gln Val Glu Lys Tyr Lys Leu Asp Ile Ala
      245            250            255
Gln Leu Glu Glu Asn Leu Lys Glu Lys Asn Asp Glu Ile Leu Ser Leu
      260            265            270
Lys Gln Ser Leu Glu Asp Asn Ile Val Ile Leu Ser Lys Gln Val Glu
      275            280            285
Asp Leu Asn Val Lys Cys Gln Leu Leu Glu Thr Glu Lys Glu Asp His
      290            295            300

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Val Asn Arg Asn Arg Glu His Asn Glu Asn Leu Asn Ala Glu Met Gln
 305 310 315 320
 Asn Leu Glu Gln Lys Phe Ile Leu Glu Gln Arg Glu His Glu Lys Leu
 325 330 335
 Gln Gln Lys Glu Leu Gln Ile Asp Ser Leu Leu Gln Gln Glu Lys Glu
 340 345 350
 Leu Ser Ser Ser Leu His Gln Lys Leu Cys Ser Phe Gln Glu Glu Met
 355 360 365
 Val Lys Glu Lys Asn Leu Phe Glu Glu Glu Leu Lys Gln Thr Leu Asp
 370 375 380
 Glu Leu Asp Lys Leu Gln Lys Glu Glu Gln Ala Glu Arg Leu Val
 385 390 395 400
 Lys Gln Leu Glu Glu Ala Lys Ser Arg Ala Glu Glu Leu Lys Leu
 405 410 415
 Leu Glu Glu Lys Leu Lys Gly Lys Glu Ala Glu Leu Glu Lys Ser Ser
 420 425 430
 Ala Ala His Thr Gln Ala Thr Leu Leu Leu Gln Glu Lys Tyr Asp Ser
 435 440 445
 Met Val Gln Ser Leu Glu Asp Val Thr Ala Gln Phe Glu Ser Tyr Lys
 450 455 460
 Ala Leu Thr Ala Ser Glu Ile Glu Asp Leu Lys Leu Glu Asn Ser Ser
 465 470 475 480
 Leu Gln Glu Lys Ala Ala Lys Ala Gly Lys Asn Ala Glu Asp Val Gln
 485 490 495
 His Gln Ile Leu Ala Thr Glu Ser Ser Asn Gln Glu Tyr Val Arg Met
 500 505 510
 Leu Leu Asp Leu Gln Thr Lys Ser Ala Leu Lys Glu Thr Glu Ile Lys
 515 520 525
 Glu Ile Thr Val Ser Phe Leu Gln Lys Ile Thr Asp Leu Gln Asn Gln
 530 535 540
 Leu Lys Gln Gln Glu Glu Asp Phe Arg Lys Gln Leu Glu Asp Glu Glu
 545 550 555 560
 Gly Arg Lys Ala Glu Lys Glu Asn Thr Thr Ala Glu Leu Thr Glu Glu
 565 570 575
 Ile Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Asn Lys Thr Lys
 580 585 590
 Pro Phe Gln Leu Gln Leu Asp Ala Phe Glu Val Glu Lys Gln Ala Leu
 595 600 605
 Leu Asn Glu His Gly Ala Ala Gln Glu Gln Leu Asn Lys Ile Arg Asp
 610 615 620
 Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys
 625 630 635 640
 His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val
 645 650 655
 Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Lys Gln Ser Glu Thr Lys
 660 665 670
 Leu Gln Glu Glu Leu Asn Lys Val Leu Gly Ile Lys His Phe Asp Pro
 675 680 685
 Ser Lys Ala Phe His His Glu Ser Lys Glu Asn Phe Ala Leu Lys Thr
 690 695 700
 Pro Leu Lys Glu Gly Asn Thr Asn Cys Tyr Arg Ala Pro Met Glu Cys
 705 710 715 720
 Gln Glu Ser Trp Lys
 725

<210> 16

<211> 2756

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 16

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atgtcctttc	ctaaggcgcc	cttgaaacga	ttcaatgacc	cttctgggtg	tgcaccatct	120
ccagggtgctt	atgatgttaa	aacttttagaa	gtattgaaag	gaccagtatc	ctttcagaaa	180
tcacaaagat	ttaaacaaca	aaaagaatct	aaacaaaatc	ttaatgttga	caaagatact	240
accttgccctg	cttcagctag	aaaagttaag	tcttcggaat	caaagaagga	atctcaaaag	300
aatgataaag	atttgaagat	attagagaaa	gagattcgtg	ttcttctaca	ggaacgtggt	360
gcccaggaca	ggcggatcca	ggatctggaa	actgagttgg	aaaagatgga	agcaaggcta	420
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cttattgaat	tgaccaggac	taatgaacta	ctaaaatcta	agttttctga	aaatggtaac	540
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aagatgaggg	gtatgatggc	taagcaagaa	ggcatggaga	tgaagctgca	ggtcacccaa	660
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gagaaagaaa	agattgatga	aaaatctgaa	acagaaaaac	tcttggaata	catcgaagaa	780
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tttgaagtag	aaaaacaggc	attgttgaat	gaacatgggtg	cagctcagga	acagctaaat	1920
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catgtttgtga	agttgaaaga	tgaaaatagc	caactcaaat	cggaggtatc	aaaactccgc	2040
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ctagggtatca	aacactttga	tccttcaaag	gcttttcatc	atgaaagtta	agaaaaat	2160
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tcttgagggc	ttttctagtc	tgagcttctt	tagctaggct	aaaacacctt	ggcttggtat	2640
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<210> 17

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 17

```

Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
 1           5           10           15
Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu
          20           25           30
Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu
          35           40           45
Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
    50           55

```

<210> 18

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 18

```

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1           5           10           15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
          20           25           30
Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
          35           40           45
Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
    50           55           60

```

<210> 19

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 19

```

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1           5           10           15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
          20           25           30
Glu Val Ser Lys Leu Arg Ser Gln Leu Lys Arg Lys Gln Asn Glu Leu
          35           40           45
Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
    50           55

```

<210> 20

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

```

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1           5           10           15

```


Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
 20 25 30
 Glu Val Ser Lys Leu Arg Ser Gln Leu Ala Lys Arg Lys Gln Asn Glu
 35 40 45
 Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
 50 55 60

<210> 21

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 21

Arg Asp Ser Tyr Ala Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
 1 5 10 15
 Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu
 20 25 30
 Val Ser Lys Leu Arg Gln Leu Lys Lys Gln Glu Leu Gln Glu Leu Lys
 35 40 45
 Leu Gly
 50

<210> 22

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 22

Arg Asp Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1 5 10 15
 Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
 20 25 30
 Glu Val Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Lys Gln Ser Glu
 35 40 45
 Thr Lys Leu Gln Glu Glu Leu Asn Lys Val Leu Gly
 50 55 60

<210> 23

<211> 49

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 23

Arg Asp Ser Tyr Ala Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
 1 5 10 15
 Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Leu Lys Ser Glu Val
 20 25 30
 Lys Leu Arg Gln Leu Lys Arg Lys Gln Glu Leu Gln Glu Leu Lys Leu
 35 40 45

Gly

<210> 24
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 24
 Arg Asp Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1 5 10 15
 Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Asn Leu Lys Ser
 20 25 30
 Glu Val Leu Lys Leu Arg Ala Gln Leu Thr Lys Arg Lys Gln Ser Glu
 35 40 45
 Ala Lys Leu Gln Glu Glu Leu Asn Lys Val Leu Gly
 50 55 60

<210> 25
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 25
 Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys
 1 5 10 15
 His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val
 20 25 30
 Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg
 35 40 45
 Leu Gln
 50

<210> 26
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 26
 Tyr Ala Leu Gly His Gln Asn Gln Lys Ile Lys His Val Lys Leu Lys
 1 5 10 15
 Glu Asn Leu Lys Glu Val Ser Lys Leu Arg Ser Gln Lys Lys Gln Arg
 20 25 30
 Leu

<210> 27
 <211> 50
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 27

```

Ala Tyr Ala Asn Leu Met Gly His Gln Asn Gln Arg Gln Lys Ile Lys
 1             5             10             15
His Met Val Lys Leu Lys Glu Glu Asn Leu Glu Leu Lys Gln Glu Val
      20             25             30
Ser Lys Leu Arg Ser Gln Val Gly Lys Gln Lys Gln Glu Leu Asp Arg
   35             40             45
Leu Lys
   50

```

<210> 28

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 28

```

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1             5             10             15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
      20             25             30

```

<210> 29

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 29

```

Leu Lys Ser Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys
 1             5             10             15
Gln Asn Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile
      20             25             30
Arg

```

<210> 30

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 30

```

Leu Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn
 1             5             10             15

```

Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg
 20 25 30

<210> 31

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 31

Leu Ser Gln Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys
 1 5 10 15
 Gln Asn Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile
 20 25 30
 Arg

<210> 32

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 32

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1 5 10 15
 Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
 20 25 30
 Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys
 35 40

<210> 33

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 33

Arg Asp Ser Tyr Ala Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
 1 5 10 15
 Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Val
 20 25 30
 Lys Lys

<210> 34

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 34

```
Arg Asp Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys
 1           5           10           15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
          20           25           30
Val Cys Lys Met Thr Phe His Phe Ile Lys
      35           40
```

<210> 35

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 35

```
Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
 1           5           10           15
Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg
          20           25           30
```

<210> 36

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 36

```
Glu Val Ser Lys Leu Arg Gln Leu Lys Lys Gln Glu Leu Gln Glu Leu
 1           5           10           15
Lys Leu Gly Ile
      20
```

<210> 37

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 37

```
Glu Val Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Lys Gln Ser Glu
 1           5           10           15
Thr Lys Leu Gln Glu Glu Leu Asn Lys Val Leu Gly Ile Lys
          20           25           30
```

<210> 38

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 38

Tyr	Ala	Leu	Leu	Gly	His	Gln	Asn	Lys	Gln	Lys	Ile	His	Lys	Lys	Asp
1				5				10						15	
Glu	Asn	Leu	Lys	Glu	Val	Lys	Leu	Arg	Lys	Asn	Gly				
		20						25							

<210> 39

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 39

Asn	Asp	Tyr	Ala	Lys	Leu	Leu	Gly	His	Gln	Asn	Gln	Lys	Gln	Lys	Ile
1				5				10					15		
His	His	Ile	Met	Lys	Ile	Lys	Asp	Glu	Asn	Ala	Ser	Leu	Lys	Lys	Glu
			20					25					30		
Val	Thr	Lys	Leu	Arg	Glu	Glu	Thr	Thr	Lys	Gln	Ser	Arg	Asn	Leu	Arg
		35					40					45			
Gln	Met	Lys	Asp	Lys	Val	Glu	Lys	Met	Glu	Gly					
	50						55								

<210> 40

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 40

Asp	Ser	Tyr	Ala	Gln	Leu	Leu	Gly	His	Gln	Asn	Leu	Lys	Gln	Lys	Ile
1				5				10					15		
Lys	His	Val	Val	Lys	Leu	Lys	Asp	Glu	Asn	Ser	Gln	Leu	Lys		
		20						25				30			

<210> 41

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 41

Asp	Tyr	Ala	Leu	Gly	His	Gln	Asn	Gln	Lys	Ile	Lys	His	Val	Lys	Leu
1				5				10					15		
Lys	Glu	Asn	Leu	Lys											
		20													

<210> 42

<211> 30

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42

Asp	Ala	Tyr	Ala	Asn	Leu	Met	Gly	His	Gln	Asn	Gln	Arg	Gln	Lys	Ile
1				5					10					15	
Lys	His	Met	Val	Lys	Leu	Lys	Glu	Glu	Asn	Leu	Glu	Leu	Lys		
			20				25						30		

<210> 43

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43

Glu	Val	Ser	Lys	Leu	Arg	Ser	Gln	Leu	Val	Lys	Arg	Lys	Gln	Asn	Glu
1				5				10						15	
Leu	Arg	Leu	Gln												
			20												

<210> 44

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 44

Glu	Val	Ser	Lys	Leu	Arg	Ser	Gln	Lys	Lys	Gln	Arg	Leu
1				5				10				

<210> 45

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 45

Glu	Val	Ser	Lys	Leu	Arg	Ser	Gln	Val	Gly	Lys	Gln	Lys	Gln	Glu	Leu
1				5				10						15	
Asp	Arg	Leu	Lys												
			20												

<210> 46

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 46

Gln	Leu	Leu	Gly	His	Gln	Asn	Leu	Lys	Gln	Lys	Ile	Lys	His	Val	Val
1				5					10					15	
Lys	Leu	Lys	Asp	Glu	Asn	Ser	Gln	Leu	Lys	Ser	Glu	Val	Ser	Lys	Leu
			20					25					30		
Arg	Ser	Gln	Leu	Val	Lys	Arg	Lys	Gln	Asn	Glu					
			35					40							

<210> 47

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 47

Leu	Gly	His	Gln	Asn	Leu	Gln	Lys	Ile	Val	Val	Leu	Lys	Glu	Asn	Leu
1				5					10					15	
Glu	Lys	Leu	Arg	Val	Lys										
			20												

<210> 48

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 48

Lys	Leu	Ile	Gly	His	Gln	Asn	Leu	His	Gln	Lys	Ile	Gln	Tyr	Val	Val
1				5					10					15	
Arg	Leu	Lys	Lys	Glu	Asn	Ile	Arg	Leu	Ala	Glu	Glu	Thr	Glu	Lys	Leu
			20					25					30		
Arg	Ala	Glu	Asn	Val	Phe	Leu	Lys	Glu	Arg	Lys					
			35					40							

<210> 49

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 49

Leu	Gly	His	Gln	Asn	Leu	Gln	Lys	Ile	Val	Val	Leu	Lys	Glu	Asn	Leu
1				5					10					15	
Glu	Lys	Leu	Arg	Val	Lys										
			20												

<210> 50

<211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 50
 Lys Leu Val Gly His Gln Asn Leu His Gln Lys Ile Gln Tyr Val Val
 1 5 10 15
 Arg Leu Lys Lys Glu Asn Val Arg Leu Ala Glu Glu Thr Glu Lys Leu
 20 25 30
 Arg Ala Glu Asn Val Phe Leu Lys Glu Lys Lys
 35 40

<210> 51
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 51
 Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys His Val Val
 1 5 10 15
 Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser Lys Leu
 20 25 30
 Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
 35 40

<210> 52
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 52
 Leu Gly His Gln Asn Leu Gln Lys Ile Val Val Leu Lys Glu Asn Leu
 1 5 10 15
 Glu Lys Leu Arg Lys Lys Glu
 20

<210> 53
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 53
 Lys Leu Val Gly His Gln Asn Leu His Gln Lys Ile Gln Tyr Val Val
 1 5 10 15

Arg Leu Lys Lys Glu Asn Ile Arg Leu Thr Glu Glu Thr Glu Lys Leu
 20 25 30
 Arg Ala Glu Asn Leu Phe Leu Lys Glu Lys Lys Lys Glu
 35 40 45

<210> 54
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 54
 Leu Gly His Gln Asn Gln Lys Ile Val Lys Leu Lys Glu Asn Leu Glu
 1 5 10 15
 Lys Leu Arg Lys
 20

<210> 55
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 55
 Lys Ile Leu Gly His Gln Asn Pro Asn Gln Lys Ile Gln Tyr Leu Val
 1 5 10 15
 Lys Leu Lys Lys Glu Asn Asn Lys Leu Leu Glu Glu Ala Glu Lys Leu
 20 25 30
 Arg Ile Glu Asn Leu Phe Leu Lys Glu Ser Lys
 35 40

<210> 56
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 56
 Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys His Val Val
 1 5 10 15
 Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser Lys Leu
 20 25 30
 Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg Leu Gln Gly
 35 40 45
 Glu Leu Asp
 50

<210> 57
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 57

Leu	Gly	His	Gln	Asn	Lys	Gln	Lys	Ile	His	Lys	Glu	Asn	Leu	Lys	Glu
1				5				10					15		
Val	Leu	Gln	Leu	Lys											
				20											

<210> 58

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 58

Glu	Leu	Gly	Gly	His	Gln	Asn	Pro	Lys	Gln	Lys	Ile	His	His	Leu	Gln
1				5				10						15	
Ala	Val	Lys	Ser	Glu	Asn	Tyr	Phe	Leu	Lys	Glu	Glu	Val	Glu	Ser	Leu
			20					25					30		
Glu	Lys	Gln	Leu	Gly	Lys	Ala	Gln	Ser	Asp	Ser	Glu	Gln	Met	Lys	Arg
		35					40					45			
Asp	Tyr	Glu													
		50													

<210> 59

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 59

Gln	Leu	Leu	Gly	His	Gln	Asn	Leu	Lys	Gln	Lys	Ile	Lys	His	Val	Val
1				5				10						15	
Lys	Leu	Lys	Asp	Glu	Asn	Ser	Gln	Leu							
			20					25							

<210> 60

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 60

Leu	Gly	His	Gln	Asn	Leu	Gln	Lys	Ile	Val	Val	Leu	Lys	Glu	Asn	Leu
1				5				10					15		

<210> 61

<211> 25

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 61
 Lys Leu Val Gly His Gln Asn Leu His Gln Lys Ile Gln Tyr Val Val
 1 5 10 15
 Arg Leu Lys Lys Glu Asn Val Arg Leu
 20 25

<210> 62
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 62
 Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser Lys
 1 5 10 15
 Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg
 20 25 30

<210> 63
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 63
 Val Lys Leu Glu Asn Leu Lys Lys Leu Leu Lys Gln Glu Arg
 1 5 10

<210> 64
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 64
 Val Lys Leu Glu Glu Glu Asn Arg Ser Leu Lys Ala Asp Leu Gln Lys
 1 5 10 15
 Leu Lys Asp Glu Leu Ala Ser Thr Lys Gln Ser Glu Ala Arg
 20 25 30

<210> 65
 <211> 28
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 65

Val	Lys	Leu	Lys	Asp	Glu	Asn	Ser	Gln	Leu	Lys	Ser	Glu	Val	Ser	Lys
1				5					10					15	
Leu	Arg	Ser	Gln	Leu	Val	Lys	Arg	Lys	Gln	Asn	Glu				
			20					25							

<210> 66

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 66

Val	Lys	Leu	Glu	Asn	Leu	Lys	Glu	Lys	Leu	Leu	Lys	Gln	Glu
1				5					10				

<210> 67

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 67

Val	Lys	Leu	Glu	Glu	Glu	Asn	Arg	Ser	Leu	Lys	Ala	Glu	Leu	Gln	Lys
1				5					10					15	
Leu	Lys	Asp	Glu	Leu	Ala	Ser	Thr	Lys	Gln	Ser	Glu				
			20					25							